



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 102297

TO: Phillip Gambel
Location: 8b03 / 9e12
Tuesday, August 26, 2003
Art Unit: 1644
Phone: 308-3997
Serial Number: 09 / 454651

From: Jan Delaval
Location: Biotech-Chem Library
CM1-1E07
Phone: 308-4498

jan.delaval@uspto.gov

Search Notes

10229X

Delaval, Jan

From: Gambel, Phillip
Sent: Tuesday, August 26, 2003 9:27 AM
To: Delaval, Jan
Subject: 09 / 454,651 ifw amd

jan

please perform a sequence and a sequence interference search for

ussn 09/ 454,651 (ifw amd)

SEQ ID NO: 23

thanx

phillip gambel
art unit 1644
308-3997

1644 mailbox 9e12

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name _____ Examiner #: _____ Date: _____
 Art Unit _____ Phone Number 30 _____ Serial Number: _____
 Mail Box and Bldg Room Location _____ Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc. if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

**For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

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 Date Time slot: 8/26/03
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 Client Prep Time: 10
 Total Time: 20

Type of Search

NA Sequence (#) _____
 AA Sequence (#) ☒ _____
 Structure (#) _____
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Vendors and cost where applicable

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 Other _____

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OM protein - protein search, using sw model

Run on: August 26, 2003, 10:18:32 ; Search time 39 Seconds

(without alignments)
532.627 Million cell updates/sec

Title: US-09-454-651B-23

Perfect score: 1149

Sequence: 1 GLSHFCGVIHVTKEVKEVA.....LRVQNTFNWNTTQEHFPDN 216

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 segs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 76: *
1: PIR1: *
2: PIR2: *
3: PIR3: *
4: PIR4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1149	100.0	288	A45803	B-cell-restricted
2	1085	94.4	289	G00031	B7 protein - red-c
3	738	64.2	299	I46690	CD80 precursor - r
4	601.5	52.3	321	I54766	B-lymphocyte activ
5	561	48.8	309	I49503	B-lymphocyte activ
6	185	16.1	275	JC7604	CD86 spliced varia
7	182	15.8	329	I48754	B7-2 antigen - hum
8	152	13.2	309	I49522	gene B7-2 protein
9	140.5	12.2	330	I46691	CD86 precursor - r
10	133.5	11.6	583	I39428	alcam - human
11	129	11.2	221	Q0BB48	BARF1 protein - hu
12	127	11.1	526	J70587	butyrophilin precu
13	122.5	10.7	588	JH0506	adhesion molecule
14	122.5	10.7	588	A45254	surface glycoprote
15	120.5	10.5	509	JC5288	SHP substrate-1 pr
16	120.5	10.5	513	JC5289	SHP substrate-1 pr
17	118	10.3	487	S65133	butyrophilin - mou
18	116.5	10.1	1088	I3XLNL	neural cell adhesi
19	115	10.0	761	I3HJNG	neural cell adhesi
20	112.5	9.8	725	JE0099	neural cell adhesi
21	110.5	9.6	587	JH0464	DM-GRASP precursor
22	109.5	9.5	646	I38049	cell surface glyco
23	109.5	9.5	853	I3B0NC	neural cell adhesi
24	109	9.5	526	A37821	butyrophilin - bov
25	109	9.5	2029	1 TDFELK	protein-tyrosine-p
26	108	9.4	871	I48696	protein-tyrosine k
27	108	9.4	881	I48697	protein-tyrosine k
28	107.5	9.4	5175	T20992	hypothetical prote
29	107.5	9.4	5198	T43290	hemiscentin precurs

30 106.5 9.3 333 2 A31923
31 106.5 9.3 858 1 IJRTNC
32 106 9.2 267 2 PJ0064
33 105.5 9.2 1091 1 IJCHNL
34 104.5 9.1 210 2 A56169
35 104 9.1 307 1 RWM5BC
36 104 9.1 725 2 JE0100
37 104 9.1 1092 1 JN0635
38 103.5 9.0 480 2 A56182
39 103.5 9.0 725 1 IJMSNG
40 103.5 9.0 1115 1 IJMSNL
41 103 9.0 423 2 T29549
42 103 9.0 1273 2 T42405
43 102.5 8.9 503 2 JC5287
44 102 8.9 1443 2 I50600
45 101 8.8 1033 2 S19247

ALIGNMENTS

RESULT 1

A45803

B-cell-restricted antigen B7 precursor - human

N:Alternate names: B-lymphocyte activation antigen B7

C:Species: Homo sapiens (man)

C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 29-Sep-1999

C:Accession: I54495; A45803

R:Selvakumar, A.; Mohanraj, B.K.; Eddy, R.L.; Shows, T.B.; White, P.C.; Dupont, B.

Immunogenetics 36, 175-181, 1992

A:Title: Genomic organization and chromosomal location of the human gene encoding the B-1

A:Reference number: 154495; MUID:92307753; PMID:1377173

A:Accession: I54495

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-288 <RES>

A:Cross-references: GB:M83077; NID:g179327; PIDN:AAA58390.1; PID:g179329

R:Freeman, G.J.; Freedman, A.S.; Segil, J.M.; Lee, G.; Whitman, J.F.; Nadler, L.M.

J. Immunol. 143, 2714-2722, 1989

A:Title: B7, a new member of the Ig superfamily with unique expression on activated and i

A:Reference number: A45803; MUID:90010147; PMID:2794510

A:Accession: A45803

A:Molecule type: mRNA

A:Residues: 1-288 <FRE>

A:Cross-references: GB:M27533; NID:g184680; PIDN:AAA36045.1; PID:g306916

C:Genetics:

A:Gene: GDB:CD80; CD28LGL1; CD28

A:Cross-references: GDB:251792; OMIM:112203

A:Map position: 3q13.3-3q21

A:Introns: 34/1; 140/1; 234/1; 266/1

C:Superfamily: B-lymphocyte restricted antigen B7

C:Keywords: transmembrane protein

F:1-26/Domain: signal sequence #status predicted <SIG>

F:248-264/Domain: transmembrane #status predicted <TM>

Query Match 100.0%; Score 1149; DB 2; Length 288;

Best Local Similarity 100.0%; Pred. No. 1.8e-85;

Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	GLSHFCGVIHVTKEVATLSCGHNVSVVEELAQTRIVQKEKKVLTNMSGDMNIWPE	60
Db	27	GLSHFCGVIHVTKEVATLSCGHNVSVVEELAQTRIVQKEKKVLTNMSGDMNIWPE	86
QY	61	YKNRTIFDITNLSIVILALRPSDEGTVCVVLKYEKDAFKREHLAEVTLVSKADFTPTS	120
Db	87	YKNRTIFDITNLSIVILALRPSDEGTVCVVLKYEKDAFKREHLAEVTLVSKADFTPTS	146
QY	121	ISDFEPTSNIRRIICSTGGPPEPHLSWLENGEELNAINTTVVSQDPETELVAVSSKLDLF	180
Db	147	ISDFEPTSNIRRIICSTGGPPEPHLSWLENGEELNAINTTVVSQDPETELVAVSSKLDLF	206
QY	181	NMTTNHSEWCLIKYGLRVNQTFNNTTQEHFPDN	216

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Db      207 MMTNHSFMCLIKYGLRLVNTQFNWNTTKQEHFPDN 242

RESULT 2
G00031
B7 protein - red-crowned mangabey (fragment)
C:Species: Cercopithecus torquatus (red-crowned mangabey, white-collared mangabey)
C:Date: 11-Apr-1997 #sequence_revision 11-Apr-1997 #text_change 29-Sep-1999
C:Accession: G00031
R:Villinger, F.J.
submitted to the EMBL Data Library, January 1995
A:Reference number: G000217
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Accession: G00031
A:Molecule type: mRNA
A:Residues: 1-289 <VIL>
A:Cross-references: EMBL:U19833; NID:G644783; PIDN:AAA86700.1; PID:G644784
C:Genetics:
A:Gene: B7
C:Superfamily: B-lymphocyte restricted antigen B7

Query Match      94.4%; Score 1085; DB 2; Length 289;
Best Local Similarity 95.3%; Pred. No. 2.7e-80;
Matches 205; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY      2 LSHFCGVIHVTKEVATLSCGHNVSVBELAQTRIVYQKEKKWLTMMSGDNNIWP 61
DB      28 LSHFCGVIHVTKEVATLSCGHNVSVBELAQTRIVYQKEKKWLTMMSGDNNIWP 87
QY      62 KNRITFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLVKADFPPTSI 121
DB      88 KNRITFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLVKADFPPTSI 147
QY      122 SDFEIPTSNIRIICSTGGPPEPHLSWLENGEELNAINTVSQDPETELYAVSKLDFN 181
DB      148 TDFEIPPSNIRIICSTGGPPEPHLSWLENGELNADITTSQDPETELYAVSKLDFN 207
QY      182 MTTNHSFMCLIKYGLRLVNTQFNWNTTKQEHFPDN 216
DB      208 MTTNHSFMCLIKYGLRLVNTQFNWNTTKQEHFPDN 242

RESULT 3
146690
CD80 precursor - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 29-Sep-1999
C:Accession: I46690
R:Isono, T.; Seto, A.
Immunogenetics 42, 217-220, 1995
A:Title: Cloning and sequencing of the rabbit gene encoding T-cell costimulatory molecule
A:Reference number: I46689; MUID:95369849; PMID:7642234
A:Accession: I46690
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-299 <ISO>
A:Cross-references: GB:D49843; NID:G755096; PIDN:BA08643.1; PID:G755097
C:Superfamily: B-lymphocyte restricted antigen B7

Query Match      64.2%; Score 738; DB 2; Length 299;
Best Local Similarity 63.9%; Pred. No. 3e-52;
Matches 133; Conservative 36; Mismatches 39; Indels 0; Gaps 0;

QY      4 HFCGVIHVTKEVATLSCGHNVSVBELAQTRIVYQKEKKWLTMMSGDNNIWP 63
DB      29 HFSSGISQVTKSVKMAALSCDYNISDELARIRIYQKQKVLISITSGVEVWPEYKN 88
QY      64 RTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLVKADFPPTSI 123
DB      89 RTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLVKADFPPTSI 148
QY      124 FEIPTSNIIRIICSTGGPPEPHLSWLENGEELNAINTVSQDPETELYAVSKLDFNMT 183
DB      148 FEIPTSNIIRIICSTGGPPEPHLSWLENGEELNAINTVSQDPETELYAVSKLDFNMT 183

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Db      149 IGHDPNVKIRCSASGGFPPEPLANWDEELNAVNTTVQDLDTELYSVSSSELDNFNT 208

QY      184 TNHSFMCLIKYGLRLVNTQFNWNTTKQEH 211
DB      209 NNHSIVCLIKYGLSVSQIFPWSKPKQEH 236

RESULT 4
154766
B-lymphocyte activation antigen 7-1 precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 19-May-2000
C:Accession: I54766
R:Judge, T.A.; Liu, M.; Christensen, P.J.; Fak, J.J.; Turka, L.A.
Int. Immunol. 7, 171-178, 1995
A:Title: Cloning the rat homolog of the CD28/CTLA-4-ligand B7-1: structural and functional
A:Reference number: I54766; MUID:95252184; PMID:7537533
A:Accession: I54766
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-321 <RES>
A:Cross-references: EMBL:U05593; NID:G453381; PIDN:AAA80154.1; PID:G453382
C:Superfamily: B-lymphocyte restricted antigen B7

Query Match      52.3%; Score 601.5; DB 2; Length 321;
Best Local Similarity 54.4%; Pred. No. 3.4e-41;
Matches 112; Conservative 35; Mismatches 58; Indels 1; Gaps 1;

QY      1 GLSHFCGVIHVTKEVATLSCGHNVSVBELAQTRIVYQKEKKWLTMMSGDNNIWP 59
DB      31 GLLOISGIVGQSVKSVREKALLSCDYKFCSEQSIHRIYQKDKVLSVIGVPEVWP 90
QY      60 EYKNTTFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLVKADFPPT 119
DB      91 KYKNTTFDITANNVFSLLGLISDRGTTCVQVYEGGSSVVKHLLTVLSVRADEPTP 150
QY      120 SISDFEIPTSNIRIICSTGGPPEPHLSWLENGEELNAINTVSQDPETELYAVSKL 179
DB      151 NITEYGNPSADIKRITCFASGFPKPLSLWLENGELNINTTISQDPESSELYTIS 210
QY      180 PMTNTNHSFMCLIKYGLRLVNTQFNWNT 205
DB      211 FNATYDHFIDCFIEYGDARVSNQFTW 236

RESULT 5
149503
B-lymphocyte activation antigen 7 precursor - mouse
N:Alternate names: MB7-2
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 29-Sep-1999
C:Accession: I49503; S17291; I49521
R:Selvakumar, A.; White, P.C.; Dupont, B.
Immunogenetics 38, 292-295, 1993
A:Title: Genomic organization of the murine B-lymphocyte activation antigen B7.
A:Reference number: I49503; MUID:93307789; PMID:7686531
A:Accession: I49503
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-309 <RES>
A:Cross-references: GB:L12589; NID:G293299; PIDN:AAA37240.1; PID:G293301
R:Freeman, G.J.; Gray, G.S.; Glimi, C.D.; Lombard, D.B.; Zhou, L.J.; White, M.; Fingerot,
J. Exp. Med. 174, 625-631, 1991
A:Title: Structure, expression, and T cell costimulatory activity of the murine homologue
A:Reference number: S17291; MUID:91341422; PMID:1714935
A:Accession: S17291
A:Molecule type: mRNA
A:Residues: 1-274, 'R', 279-309 <PRE>
A:Cross-references: EMBL:X60958; NID:G50111; PIDN:CAA43291.1; PID:G50112
R:Inobe, M.; Linsley, P.S.; Ledbetter, J.A.; Nagai, Y.; Tamakoshi, M.; Ueda, T.
Biochem. Biophys. Res. Commun. 200, 443-449, 1994
A:Title: Identification of an alternatively spliced form of the murine homologue of B7.
A:Reference number: I49521; MUID:94220123; PMID:7513163

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OM protein - protein search, using sw model

Run on: August 26, 2003, 10:17:12 ; Search time 23 Seconds

(without alignments)
441.642 Million cell updates/sec

Title: US-09-454-651B-23

Perfect score: 1149

Sequence: 1 GLSHFPCSGVIHVKVEVA.....LRVNQTFNWNNTKQEHFPDN 216

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1149	100.0	288	1	CD80 HUMAN
2	738	64.2	299	1	CD80 RABIT
3	561	48.8	306	1	CD80 MOUSE
4	182	15.8	329	1	CD86 HUMAN
5	161	14.0	302	1	ICOL HUMAN
6	152	13.2	309	1	CD86 MOUSE
7	150.5	13.1	322	1	ICOL MOUSE
8	140.5	12.2	330	1	CD86 RABBIT
9	138	12.0	509	1	SHS1 RAT
10	134.5	11.7	583	1	C166 MOUSE
11	133.5	11.6	583	1	C166 HUMAN
12	129	11.2	221	1	BRF1 EBV
13	127	11.1	526	1	BUTY HUMAN
14	122.5	10.7	588	1	C166 CHICK
15	120.5	10.5	513	1	SHS1 MOUSE
16	120	10.4	506	1	SHS1 BOVIN
17	119	10.4	524	1	BUTY MOUSE
18	116.5	10.1	1088	1	NCA1_XENLA
19	115	10.0	761	1	NCA1_HUMAN
20	115	10.0	848	1	NCA1_HUMAN
21	110.5	9.6	321	1	TCB FLV
22	110	9.6	398	1	SRB1 HUMAN
23	109.5	9.5	646	1	MU18 HUMAN
24	109.5	9.5	853	1	NCA1_BOVIN
25	109	9.5	387	1	SRB2 HUMAN
26	109	9.5	526	1	BUTY BOVIN
27	109	9.5	2029	1	LAR DROME
28	108.5	9.4	365	1	CXAR MOUSE
29	107.5	9.4	333	1	AMAL DROME
30	106.5	9.3	858	1	NCA1 RAT
31	105	9.1	319	1	A33_HUMAN
32	105	9.1	1091	1	NCA1_CHICK
33	104	9.1	1092	1	NCA2_XENLA

34	103.5	9.0	725	1	NCA2 MOUSE
35	103.5	9.0	1115	1	NCA1 MOUSE
36	103	9.0	298	1	JAM2_HUMAN
37	102.5	8.9	503	1	SHS1_HUMAN
38	102	8.9	1443	1	NEOL_CHICK
39	101.5	8.8	403	1	RAGE MOUSE
40	100	8.7	413	1	HEMO MANSE
41	99.5	8.7	1338	1	VGR1_HUMAN
42	98.5	8.6	365	1	CXAR_HUMAN
43	98.5	8.6	1242	1	NBN_MOUSE
44	98	8.5	278	1	OK2G_RAT
45	98	8.5	298	1	JAM1_BOVIN

P13594	mus musculus
P13595	mus musculus
P57087	homo sapien
P78324	h protein-t
Q0610	gallus gall
Q62151	mus musculus
P31398	manduca sex
P17948	h vascular
P78310	homo sapien
Q9QZS7	mus musculus
P04218	rattus norv
Q9XU56	bos taurus

ALIGNMENTS

RESULT 1	
CD80 HUMAN	CD80 HUMAN STANDARD; PRT; 288 AA.
AC P33681;	
DT 01-FEB-1994 (Rel. 28, Created)	
DT 01-FEB-1994 (Rel. 28, Last sequence update)	
DT 15-SEP-2003 (Rel. 42, Last annotation update)	
DE T lymphocyte activation antigen CD80 precursor (Activation B7-1 antigen) (CTLA-4 counter-receptor B7.1) (B7) (BB1).	
GN CD80 OR CD28LG1 OR CD28LG OR IAB7.	
OS Homo sapiens (Human).	
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
OX NCBI_TaxID=9606;	
RN [1]	SEQUENCE FROM N.A.
RP TISSUE=Lymphoid;	
RC MEDLINE=90010147; PubMed=2794510;	
RA Freeman G.J., Freedman A.S., Segil J.M., Lee G., Whitman J.F., Nadler L.M.;	
RT "B7, a new member of the Ig superfamily with unique expression on activated and neoplastic B cells.";	
RL J. Immunol. 143:2714-2722(1989).	
RN [2]	SEQUENCE FROM N.A.
RP MEDLINE=92307753; PubMed=1377173;	
RA Selvakumar A., Mohanraj B.K., Eddy R.L., Shows T.B., White P.C., Dupont B.;	
RT "Genomic organization and chromosomal location of the human gene encoding the B-lymphocyte activation antigen B7.";	
RL Immunogenetics 36:175-181(1992).	
RN [3]	SEQUENCE OF 35-38.
RP MEDLINE=91341422; PubMed=1714935;	
RA Freeman G.J., Gray G.S., Gimmi C.D., Lombard D.B., Zhou L.-J., White M., Fingerhuth J.D., Gribben J.G., Nadler L.M.;	
RT "Structure, expression, and T cell costimulatory activity of the murine homologue of the human B lymphocyte activation antigen B7.";	
RL J. Exp. Med. 174:625-631(1991).	
RN [4]	CHARACTERIZATION.
RP MEDLINE=95088403; PubMed=7527824;	
RA Lanier L.L., O'Fallon S., Somoza C., Phillips J.H., Linsley P.S., Okumura K., Ito D., Azuma M.;	
RT "CD80 (B7) and CD86 (B70) provide similar costimulatory signals for T cell proliferation, cytokine production, and generation of CTL.";	
RL J. Immunol. 154:97-105(1995).	
RN [5]	X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS) OF 35-234.
RP MEDLINE=20125021; PubMed=10661405;	
RA Ikemizu S., Gilbert R.J., Fennelly J.A., Collins A.V., Harlos K., Jones E.V., Stuart D.I., Davis S.J.;	
RT "Structure and dimerization of a soluble form of B7-1.";	
RL Immunity 12:51-60(2000).	
CC -!- FUNCTION: INVOLVED IN THE COSTIMULATORY SIGNAL ESSENTIAL FOR T LYMPHOCYTES ACTIVATION. T CELL PROLIFERATION AND CYTOKINE	

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OM protein - protein search, using sw model

Run on: August 26, 2003, 10:17:57 ; Search time 96 Seconds

(without alignments)
580.618 Million cell updates/sec

Title: US-09-454-651b-23

Perfect score: 1149

Sequence: 1 GLSHFCGVIHVTKVEKEVA.....LRVNTFNWNTKQHFDPDN 216

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1118	97.3	288	6	O77684
2	1100	95.7	288	6	Q28499
3	1085	94.4	288	6	Q9BDN6
4	1085	94.4	289	6	Q28347
5	772	67.2	296	6	Q8WMZ2
6	764	66.5	230	6	Q9N213
7	762.5	66.4	288	6	Q9TT70
8	762.5	66.4	297	6	Q9BE99
9	761	66.2	229	6	Q9TT71
10	743	64.7	292	6	Q9GMZ8
11	743	64.7	292	6	Q02758
12	719	62.6	304	6	Q9TOX1
13	717.5	62.4	296	6	Q46405
14	705	61.4	235	6	Q9N070
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16	659	57.4	294	11	Q8BH36

17	603.5	52.5	321	11	O35187
18	602	52.4	290	11	Q62680
19	601.5	52.3	321	11	Q62624
20	596	51.9	321	11	O55202
21	560	48.7	306	11	Q9RI29
22	350	30.5	174	6	Q9GMZ9
23	349.5	30.4	173	6	Q9SL17
24	255.5	22.2	212	11	O61332
25	200.5	17.4	329	6	Q9XSX6
26	200.5	17.4	332	6	Q9GMZ7
27	200.5	17.4	332	6	Q9SL16
28	188.5	16.4	280	6	Q9TTF1
29	188.5	16.4	296	13	O42404
30	182	15.8	329	6	Q9TTF2
31	178	15.5	323	6	Q9BDM2
32	177	15.4	323	6	Q9BDM9
33	177	15.4	323	6	Q9BDM4
34	176	15.3	275	6	Q9BDN9
35	176	15.3	323	6	Q9BDB8
36	171	14.9	284	6	Q9GL33
37	166.5	14.5	289	11	O8K3J3
38	165	14.4	281	11	O8CJ58
39	162	14.1	313	11	O35531
40	161.5	14.1	325	6	O02838
41	159	13.8	316	11	Q9VE98
42	156.5	13.6	290	4	Q9NZQ7
43	153	13.3	290	11	Q9EP73
44	153	13.3	356	11	O64381
45	152	13.2	314	11	Q61238

ALIGNMENTS

RESULT 1

O77684
ID O77684 PRELIMINARY; PRT; 288 AA.
AC O77684;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE B7 protein.
GN B7.
OS Macaca nemestrina (Pig-tailed macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9545;
RN [1]
RP SEQUENCE FROM N.A.
RA Kraus G., Hnatyszyn J.H.;
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF079519; AAC31555.1; -
DR HSSP; P33681; 1DR9.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF000047; ig; 1.
DR SMART; SM00409; Ig; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
SQ SEQUENCE 288 AA; 33131 MW; 76B8C42839E9AB79 CRC64;

Query Match 97.3%; Score 1118; DB 6; Length 288;

Best Local Similarity 97.7%; Pred. No. 1e-92; Mismatches 4; Indels 0; Gaps 0;
Matches 210; Conservative 1;

Qy 2 LSHFCGVIHVTKVEKEVATLSCGHNVSVVEELAQTRIYNQKXKXVLTWMSGDMNIWPEY 61

Db 28 LSHFCGVIHVTKVEKEVATLSCGHNVSVVEELAQTRIYNQKXKXVLTWMSGDMNIWPEY 87

Qy 62 KNTIFDITNNLSIVIALRPPSGEGYECVVLKYEKDAFKREHLAEVTLTSVKADFTTFSI 121

Db 88 KNTIFDITNNLSIVIALRPPSGEGYECVVLKYEKDAFKREHLAEVTLTSVKADFTTFSI 147


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QY 122 SDFEPTSNIRRIICSTSGGPPPEHLVSWLNGEELNAINTTVSQDPETELYAVSSKLDEN 181
DB 148 TDFEIPPSNIRRIICSTSGGPPPEHLVSWLNGEELNAINTTVSQDPETELYAVSSKLDEN 207

QY 182 MTNHSFMCLLIKYGLRVNQTFFNNTTKQEHFPDN 216
DB 208 MTNHSFMCLLIKYGLRVNQTFFNNTPKQEHFPDN 242

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Q28499 PRELIMINARY; PRT; 288 AA.
AC Q28499;
DT 01-NOV-1996 (TREMELrel. 01, Created)
DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)
DT 01-MAR-2003 (TREMELrel. 23, Last annotation update)
DE B7 protein (CD80 protein precursor).
GN B7 OR N939.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=96003435; PubMed=7561102;
RA Villinger F., Brar S.S., Wayne A., Chikkala N., Ansari A.A.;
RT "Comparative sequence analysis of cytokine genes from human and
nonhuman primates.";
RL J. Immunol. 155:3946-3954 (1995).
RN [2]
RP SEQUENCE FROM N.A.
RA Villinger F., Bostik P., Wayne A.E., King C.L., Genain C.P.,
Weiss W.R., Ansari A.A.;
RT "Cloning, sequencing and homology analysis of nonhuman primate
Fas/Fas-Ligand and co-stimulatory molecules.";
RL Immunogenetics 0:0-0 (2001).
DR EMBL; U19840; AAA86706.1; -.
DR EMBL; AF344849; AAK37609.1; -.
DR HSSP; P33681; 1DR9.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS0835; IG_LIKE; 2.
KW SIGNAL.
FT SIGNAL.
SQ SEQUENCE 1 26 POTENTIAL.
1 26
SEQUENCE 288 AA; 33141 MW; E70BEA4006C7A609 CRC64;

Query Match 95.7%; Score 1100; DB 6; Length 288;
Best Local Similarity 96.3%; Pred. No. 4.2e-91;
Matches 207; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 2 LSHFCGVIHVTKEKVATLSCGHNVSVEELAQTRIYQKEKVMVLTWMSGDMNIWPEY 61
DB 28 LSHFCGVIHVTKEKVATLSCGHNVSVEELAQTRIYQKEKVMVLTWMSGDMNIWPEY 87

QY 62 KNRTIFDITNNLSIVILALRPSDEGYECVVLKYEKDAFKREHLAEVTLVSKADFTPSI 121
DB 88 KNRTIFDITNNLSIVILALRPSDEGYECVVLKYEKDAFKREHLAEVTLVSKADFTPSI 147

QY 122 SDFEPTSNIRRIICSTSGGPPPEHLVSWLNGEELNAINTTVSQDPETELYAVSSKLDEN 181
DB 148 TDFEIPPSNIRRIICSTSGGPPPEHLVSWLNGEELNAINTTVSQDPETELYAVSSKLDEN 207

QY 182 MTNHSFMCLLIKYGLRVNQTFFNNTTKQEHFPDN 216
DB 208 MTNHSFMCLLIKYGLRVNQTFFNNTPKQEHFPDN 242

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AC Q28347;
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DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)
DT 01-MAR-2003 (TREMELrel. 23, Last annotation update)
DE B7 protein (fragment).
GN B7.
OS Cercopithecus torquatus (red-crowned mangabey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Cercopithecus.
OX NCBI_TaxID=9530;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=96003435; PubMed=7561102;
RA Villinger F., Brar S.S., Wayne A., Chikkala N., Ansari A.A.;
RT "Comparative sequence analysis of cytokine genes from human and
nonhuman primates.";

```

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Q28DN6 PRELIMINARY; PRT; 288 AA.
AC Q28DN6;
DT 01-JUN-2001 (TREMELrel. 17, Created)
DT 01-JUN-2001 (TREMELrel. 17, Last sequence update)
DT 01-MAR-2003 (TREMELrel. 23, Last annotation update)
DE CD80 protein.
GN MNE71.
OS Cercopithecus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Cercopithecus.
OX NCBI_TaxID=9531;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21383618; PubMed=11491535;
RA Villinger F., Bostik P., Wayne A.E., King C.L., Genain C.P.,
Weiss W.R., Ansari A.A.;
RT "Cloning, sequencing, and homology analysis of nonhuman primate
Fas/Fas-Ligand and co-stimulatory molecules.";
RL Immunogenetics 53:315-328 (2001).
DR EMBL; AF344839; AAK37535.1; -.
DR HSSP; P33681; 1DR9.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS0835; IG_LIKE; 1.
SQ SEQUENCE 288 AA; 32917 MW; C6A3F6A3C592972B CRC64;

Query Match 94.4%; Score 1085; DB 6; Length 288;
Best Local Similarity 95.3%; Pred. No. 9.4e-90;
Matches 205; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

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DB 28 LSHFCGVIHVTKEKVATLSCGHNVSVEELAQTRIYQKEKVMVLTWMSGDMNIWPEY 87

QY 62 KNRTIFDITNNLSIVILALRPSDEGYECVVLKYEKDAFKREHLAEVTLVSKADFTPSI 121
DB 88 KNRTIFDITNNLSIVILALRPSDEGYECVVLKYEKDAFKREHLAEVTLVSKADFTPSI 147

QY 122 SDFEPTSNIRRIICSTSGGPPPEHLVSWLNGEELNAINTTVSQDPETELYAVSSKLDEN 181
DB 148 TDFEIPPSNIRRIICSTSGGPPPEHLVSWLNGEELNAINTTVSQDPETELYAVSSKLDEN 207

QY 182 MTNHSFMCLLIKYGLRVNQTFFNNTTKQEHFPDN 216
DB 208 MTNHSFMCLLIKYGLRVNQTFFNNTPKQEHFPDN 242

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Q28347 PRELIMINARY; PRT; 289 AA.
AC Q28347;
DT 01-NOV-1996 (TREMELrel. 01, Created)
DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)
DT 01-MAR-2003 (TREMELrel. 23, Last annotation update)
DE B7 protein (fragment).
GN B7.
OS Cercopithecus torquatus (red-crowned mangabey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Cercopithecus.
OX NCBI_TaxID=9530;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=96003435; PubMed=7561102;
RA Villinger F., Brar S.S., Wayne A., Chikkala N., Ansari A.A.;
RT "Comparative sequence analysis of cytokine genes from human and
nonhuman primates.";

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7	1.149	100.0	288	21	AAAY44289	Human B7.1 co-stim
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Freeman GJ, Gray GS, Greenfield E, Nadler LM;
 WPI; 1995-075236/10.
 N-PSDB; AAQ81371.
 Nucleic acids encoding CTLA4/CD28 counter receptor, B7-2 - useful
 for enhancing or suppressing T-cell mediated immune responses
 Disclosure; pages 111-113; 175pp; English.
 Q81371 is in pCDM8 vector. It is derived from lymphoid B cells,
 cell line Raji, clone no. 13. Its position in the genome is
 chromosome/segment 3. It was published by Freeman, F.J. et al.,
 J. of Immunology, 143: 8: 2714-2722, 15th October 1989. It can be
 found in Genbank at Accession no. M27533. The encoded protein,
 R67989, binds both human CTLA4 and human CD28. It is related
 to human hB7-2 (see Q81351) and murine hB7 (see Q81372).
 (Updated on 25-MAR-2003 to correct PN field.)

Query Match 100.0%; Score 1149; DB 16; Length 288;
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 b 27 GLSHFCGVIHVTKEVATLSGCHNVSVVEELAQRIYQKEKKVLTWMSGDMNIWPE 86
 Y 61 YKNTTFDITNNLSIVILALRPSDEGTVECVLKYEKDAFKREHLAEVTLVKADFPPTS 120
 b 87 YKNTTFDITNNLSIVILALRPSDEGTVECVLKYEKDAFKREHLAEVTLVKADFPPTS 146
 Y 121 ISDFEPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTTVSQDPETELAYVSSKIDF 180
 b 147 ISDFEPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTTVSQDPETELAYVSSKIDF 206
 Y 181 NMTNHSFMCILIKYGHRLVNOQTFNNTTKQEHFPDN 216
 b 207 NMTNHSFMCILIKYGHRLVNOQTFNNTTKQEHFPDN 242

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 ID
 D AA67804 standard; Protein; 288 AA.

XX AAW38414;
 AC 08-APR-1998 (first entry)
 DT B7-1.
 XX Screening; inhibitor; enhancer; binding; CD28; B7-1.
 KW Homo sapiens.
 OS EP795554-A2.
 PN 17-SEP-1997.
 XX 04-MAR-1997; 97EP-0301438.
 PF 02-OCT-1996; 96JP-0262085.
 PR 05-MAR-1996; 96JP-0047795.
 XX (TAKE) TAKEDA CHEM IND LTD.
 PA Hattori M, Hida T, Kurokawa T, Nakanishi A;
 XX WPI; 1997-450803/42.
 DR N-PSDB; AAT96358.
 XX New xanthene derivatives useful as immunomodulators - e.g. methyl
 PT 2-(carboxymethylsulphonyl)-5,7-dichloro-3,8-dihydroxy-6-
 PT methyl-9-oxo-9H-xanthene-1-carboxylate.
 XX Disclosure; Fig 4; 117pp; English.
 PS The present sequence was used in the development of a novel method
 CC for screening for compounds that inhibit or enhance binding of CD28
 CC to B7-1.
 CC XX
 SQ Sequence 288 AA;

Query Match 100.0%; Score 1149; DB 18; Length 288;
 Best Local Similarity 100.0%; Pred. No. 3.4e-103;
 Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 Db 27 GLSHFCGVIHVTKEVATLSGCHNVSVVEELAQRIYQKEKKVLTWMSGDMNIWPE 86
 QY 61 YKNTTFDITNNLSIVILALRPSDEGTVECVLKYEKDAFKREHLAEVTLVKADFPPTS 120
 Db 87 YKNTTFDITNNLSIVILALRPSDEGTVECVLKYEKDAFKREHLAEVTLVKADFPPTS 146
 QY 121 ISDFEPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTTVSQDPETELAYVSSKIDF 180
 Db 147 ISDFEPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTTVSQDPETELAYVSSKIDF 206
 QY 181 NMTNHSFMCILIKYGHRLVNOQTFNNTTKQEHFPDN 216
 Db 207 NMTNHSFMCILIKYGHRLVNOQTFNNTTKQEHFPDN 242

RESULT 3
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 XX AAW67804 standard; Protein; 288 AA.
 XX AAW67804;
 XX 13-APR-1999 (first entry)
 DT Human B7 protein sequence.
 DE Human; B7; transfection; mammal; tumour cell; sarcoma; co-stimulation;
 XX T- cell; CD28; CTLA4; ligand; T-lymphocyte response; metastasis.
 XX

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 26, 2003, 10:23:43 ; Search time 57 Seconds
(without alignments)

500.065 Million cell updates/sec

Title: US-09-454-651B-23

Perfect score: 1149

Sequence: 1 GLSHFCSGVIHVTKEVKEVA.....LRVNQTFNNTTKQEHFPDN 216

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 497079 seqs, 131961718 residues

Total number of hits satisfying chosen parameters: 497079

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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6	1149	100.0	288	10	US-09-896-738-10
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8	1149	100.0	288	11	US-09-962-969-19
9	1149	100.0	288	11	US-09-350-202-2
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11	1149	100.0	288	15	US-10-261-101-2
12	1149	100.0	473	10	US-09-910-059-131
13	1143	99.5	492	10	US-09-845-899A-3
14	1129	98.3	288	12	US-10-032-214-94
15	1121	97.6	288	12	US-10-032-214-69

16	1121	97.6	288	12	US-10-032-214-82	Sequence 82, Appl
17	1119	97.4	288	12	US-10-032-214-71	Sequence 71, Appl
18	1119	97.4	288	12	US-10-032-214-77	Sequence 77, Appl
19	1119	97.4	288	12	US-10-032-214-225	Sequence 225, App
20	1118	97.3	288	12	US-10-032-214-84	Sequence 84, Appl
21	1116	97.1	288	12	US-10-032-214-76	Sequence 76, Appl
22	1116	97.1	288	12	US-10-032-214-86	Sequence 86, Appl
23	1116	97.1	288	12	US-10-032-214-87	Sequence 87, Appl
24	1116	97.1	288	12	US-10-032-214-286	Sequence 286, App
25	1114	97.0	288	12	US-10-032-214-226	Sequence 226, App
26	1114	97.0	288	12	US-10-032-214-251	Sequence 251, App
27	1113	96.9	288	12	US-10-032-214-90	Sequence 90, Appl
28	1113	96.9	288	12	US-10-032-214-228	Sequence 228, App
29	1113	96.9	288	12	US-10-032-214-250	Sequence 250, App
30	1112	96.8	288	12	US-10-032-214-78	Sequence 78, Appl
31	1112	96.8	288	12	US-10-032-214-248	Sequence 248, App
32	1111	96.7	288	12	US-10-032-214-238	Sequence 238, App
33	1110	96.6	288	12	US-10-032-214-236	Sequence 236, App
34	1109	96.5	288	12	US-10-032-214-88	Sequence 88, Appl
35	1109	96.5	288	12	US-10-032-214-89	Sequence 89, Appl
36	1109	96.5	288	12	US-10-032-214-92	Sequence 92, Appl
37	1109	96.5	288	12	US-10-032-214-249	Sequence 249, App
38	1108	96.4	287	12	US-10-032-214-243	Sequence 243, App
39	1105	96.2	288	12	US-10-032-214-81	Sequence 81, Appl
40	1104	96.1	287	12	US-10-032-214-74	Sequence 74, Appl
41	1104	96.1	300	12	US-10-032-214-232	Sequence 232, App
42	1103	96.0	288	12	US-10-032-214-91	Sequence 91, Appl
43	1103	96.0	288	12	US-10-032-214-229	Sequence 229, App
44	1103	96.0	288	12	US-10-032-214-231	Sequence 231, App
45	1101	95.8	288	12	US-10-032-214-73	Sequence 73, Appl

ALIGNMENTS

RESULT 1

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US-09-915-789A-21
; Sequence 21, Application US/09915789A
; Patent No. US20020168762A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Lieping
; TITLE OF INVENTION: B7-H3 AND B7-H4, NOVEL IMMUNOREGULATORY
; MOLECULES
; FILE REFERENCE: 07039-219001
; CURRENT APPLICATION NUMBER: US/09/915,789A
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 60/220,991
; PRIOR FILING DATE: 2000-07-27
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-915-789A-21

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Query Match		100.0%;	Score 1149;	DB 10;	Length 226;
Best Local Similarity		100.0%;	Pred. No. 5.1e-103;		
Matches 216;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	GLSHFCSGVIHVTKEVKEVATLSCGHNVSVVEELAQTRIVYQKEKKVLTMMSGDMNIWPE	60		
Db	11	GLSHFCSGVIHVTKEVKEVATLSCGHNVSVVEELAQTRIVYQKEKKVLTMMSGDMNIWPE	70		
QY	61	YKNRTFIDITNNLSIVILALRSDSGTVECVLVKYKQAFKEHLEAVTLVSKADFPPTS	120		
Db	71	YKNRTFIDITNNLSIVILALRSDSGTVECVLVKYKQAFKEHLEAVTLVSKADFPPTS	130		
QY	121	ISDFEIPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTVSDPEPELVAVSKLDF	180		
Db	131	ISDFEIPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTVSDPEPELVAVSKLDF	190		
QY	181	NMTNHSFMCILIKYGLHVRVNTQFNWNTTKQEHFPDN	216		

Db 191 NM1TNHSMCLIKYCHLRVQNTFNWNTTKQBHFDPN 226

|||||

RESULT 2

US-08-592-711-2

Sequence 2, Application US/08592711

Publication No. US20020115214A1

GENERAL INFORMATION:

APPLICANT: June, Carl H.

APPLICANT: Thompson, Craig B.

APPLICANT: Nabel, Gary J.

APPLICANT: Gray, Gary S.

APPLICANT: Rennert, Paul D.

TITLE OF INVENTION: Methods For Selectively Stimulating Proliferation Of T-Cells

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE & COCKFIELD

STREET: 60 State Street

CITY: Boston

STATE: Massachusetts

COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/592,711

FILING DATE: 26-JAN-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/435,816

FILING DATE: 4-MAY-1995

APPLICATION NUMBER: US 08/403,253

FILING DATE: 10-MARCH-1995

APPLICATION NUMBER: US 08/253,964

FILING DATE: 3-JUNE-1994

APPLICATION NUMBER: US 08/073,223

FILING DATE: 4-JUNE-1993

APPLICATION NUMBER: US 08/200,947

FILING DATE: 23-FEB-1994

APPLICATION NUMBER: US 07/864,805

FILING DATE: 7-APR-1992

APPLICATION NUMBER: US 08/247,505

FILING DATE: 23-MAY-1994

APPLICATION NUMBER: US 07/864,866

FILING DATE: 7-APR-1992

APPLICATION NUMBER: US 08/218,155

FILING DATE: 25-MAR-1994

APPLICATION NUMBER: US 07/864,807

FILING DATE: 7-APR-1992

APPLICATION NUMBER: US 07/902,467

FILING DATE: 16-JUNE-1992

APPLICATION NUMBER: US 07/275,433

FILING DATE: 23-NOV-1988

ATTORNEY/AGENT INFORMATION:

NAME: Mandragoras, Amy E.

REGISTRATION NUMBER: 36,207

REFERENCE/DOCKET NUMBER: RPI-002CP4

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 227-7400

TELEFAX: (617) 227-5941

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 288 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

DESCRIPTION: B cell activation antigen; natural ligand

DESCRIPTION: for CD28 T cell surface antigen; transmembrane protein

FEATURE:

NAME/KEY: signal sequence

LOCATION: -34 to -1

IDENTIFICATION METHOD: amino terminal sequencing of

IDENTIFICATION METHOD: soluble protein

OTHER INFORMATION: hydrophobic

FEATURE:

NAME/KEY: extracellular domain

LOCATION: 1 to 208

IDENTIFICATION METHOD: similarity with known

IDENTIFICATION METHOD: sequence

FEATURE:

NAME/KEY: transmembrane domain

LOCATION: 209 to 235

IDENTIFICATION METHOD: similarity with known

IDENTIFICATION METHOD: sequence

FEATURE:

NAME/KEY: intracellular domain

LOCATION: 236 to 254

IDENTIFICATION METHOD: similarity with known

IDENTIFICATION METHOD: sequence

FEATURE:

NAME/KEY: N-linked glycosylation

LOCATION: 19 to 21

IDENTIFICATION METHOD: similarity with known

IDENTIFICATION METHOD: sequence

FEATURE:

NAME/KEY: N-linked glycosylation

LOCATION: 55 to 57

IDENTIFICATION METHOD: similarity with known

IDENTIFICATION METHOD: sequence

FEATURE:

NAME/KEY: N-linked glycosylation

LOCATION: 64 to 66

IDENTIFICATION METHOD: similarity with known

IDENTIFICATION METHOD: sequence

FEATURE:

NAME/KEY: N-linked glycosylation

LOCATION: 152 to 154

IDENTIFICATION METHOD: similarity with known

IDENTIFICATION METHOD: sequence

FEATURE:

NAME/KEY: N-linked glycosylation

LOCATION: 173 to 175

IDENTIFICATION METHOD: similarity with known

IDENTIFICATION METHOD: sequence

FEATURE:

NAME/KEY: N-linked glycosylation

LOCATION: 177 to 179

IDENTIFICATION METHOD: similarity with known

IDENTIFICATION METHOD: sequence

FEATURE:

NAME/KEY: N-linked glycosylation

LOCATION: 192 to 194

IDENTIFICATION METHOD: similarity with known

IDENTIFICATION METHOD: sequence

FEATURE:

NAME/KEY: N-linked glycosylation

LOCATION: 198 to 200

IDENTIFICATION METHOD: similarity with known

IDENTIFICATION METHOD: sequence

FEATURE:

NAME/KEY: Ig V-set domain

LOCATION: 1 to 104

IDENTIFICATION METHOD: similarity with known

IDENTIFICATION METHOD: sequence

FEATURE:

NAME/KEY: Ig C-set domain

LOCATION: 105 to 202

IDENTIFICATION METHOD: similarity with known

IDENTIFICATION METHOD: sequence

PUBLICATION INFORMATION:

AUTHORS: FREEMAN, GORDON J.

AUTHORS: FREEDMAN, ARNOLD S.

AUTHORS: SEGIL, JEFFREY M.

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

M protein - protein search, using sw model

run on: August 26, 2003, 12:18:59 ; Search time 17 Seconds

(without alignments)
537.597 Million cell updates/sec

title: US-09-454-651B-23

effect score: 1149

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coring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

searched: 328717 seqs, 42310858 residues

total number of hits satisfying chosen parameters: 328717

inimum DB seq length: 0

aximum DB seq length: 2000000000

ost-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Issued Patents AA.*
1: /cgn2_6/ptodata/1/iaa/5A.COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B.COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A.COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B.COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PTCTUS.COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match	Length	ID	Description
1	1149	100.0	288	2	US-08-147-772-2
2	1149	100.0	288	2	US-08-456-104-6
3	1149	100.0	288	2	US-08-101-624-23
4	1149	100.0	288	2	US-08-751-767A-6
5	1149	100.0	288	3	US-08-153-262-2
6	1149	100.0	288	3	US-08-479-744A-29
7	1149	100.0	288	3	US-08-280-757B-29
8	1149	100.0	288	3	US-09-159-135-2
9	1149	100.0	288	3	US-08-205-697A-19
10	1149	100.0	288	3	US-08-702-525-19
11	1149	100.0	288	4	US-09-450-798-2
12	1149	100.0	288	4	US-08-403-253A-2
13	1149	100.0	288	4	US-09-651-200-13
14	1149	100.0	288	4	US-09-667-135-34
15	1149	100.0	288	4	US-08-435-816A-2
16	1149	100.0	288	5	PCT-US95-02576-19
17	1149	100.0	473	3	US-09-171-945-131
18	1102	95.9	288	4	US-09-460-384-36
19	1100	95.7	288	4	US-09-651-200-14
20	1050	91.4	208	3	US-08-630-172-15
21	1050	91.4	208	3	US-09-375-419-15
22	743	64.7	292	4	US-09-651-200-16
23	743	64.7	292	4	US-09-303-040-2
24	739	64.3	292	4	US-09-303-040-4
25	738	64.2	299	4	US-09-651-200-15
26	561	48.8	306	3	US-08-205-697A-17
27	561	48.8	306	3	US-08-702-525-17

Sequence 17, Appl
Sequence 35, Appl
Sequence 17, Appl
Sequence 2, Appl
Sequence 2, Appl
Sequence 2, Appl
Sequence 4, Appl
Sequence 8, Appl
Sequence 25, Appl
Sequence 4, Appl
Sequence 31, Appl
Sequence 31, Appl
Sequence 4, Appl
Sequence 4, Appl
Sequence 9, Appl
Sequence 9, Appl
Sequence 11, Appl

28 561 48.8 306 4 US-09-651-200-17
29 561 48.8 306 4 US-09-667-135-35
30 561 48.8 306 5 PCT-US95-02576-17
31 561 48.8 320 3 US-08-205-697A-2
32 561 48.8 320 3 US-08-702-525-2
33 561 48.8 320 5 PCT-US95-02576-2
34 558 48.6 306 2 US-08-147-772-4
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41 558 48.6 306 4 US-09-450-798-4
42 311 27.1 200 3 US-08-205-697A-9
43 311 27.1 200 3 US-08-702-525-9
44 311 27.1 200 5 PCT-US95-02576-9
45 311 27.1 214 3 US-08-205-697A-11

ALIGNMENTS

RESULT 1
US-08-147-772-2
; Sequence 2, Application US/08147772
; Patent No. 5858776
; GENERAL INFORMATION:
; APPLICANT: Ostrand-Rosenberg, Suzanne
; APPLICANT: Baskar, Sivasubramanian
; APPLICANT: Glimcher, Laurie H.
; APPLICANT: Freeman, Gordon J.
; APPLICANT: Nadler, Lee M.
; TITLE OF INVENTION: Tumor Cells With Increased Immunogenicity
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/147,772
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragoras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: RPI-003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 288 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; DESCRIPTION: B cell activation antigen; natural ligand
; DESCRIPTION: For CD28 T cell surface antigen; transmembrane protein
; FEATURE:
; NAME/KEY: signal sequence
; LOCATION: -34 to -1
; IDENTIFICATION METHOD: amino terminal sequencing of

IDENTIFICATION METHOD: soluble protein
OTHER INFORMATION: hydrophobic
FEATURE:
NAME/KEY: extracellular domain
LOCATION: 1 to 208
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: transmembrane domain
LOCATION: 209 to 235
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: intracellular domain
LOCATION: 236 to 254
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 19 to 21
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 55 to 57
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 64 to 66
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 173 to 175
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 177 to 179
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 192 to 194
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 198 to 200
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: Ig V-set domain
LOCATION: 1 to 104
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: Ig C-set domain
LOCATION: 105 to 202
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
PUBLICATION INFORMATION:
AUTHORS: FREEMAN, GORDON J.
AUTHORS: FREEDMAN, ARNOLD S.
AUTHORS: SEGIL, JEFFREY M.
AUTHORS: LEE, GRACE
AUTHORS: WHITMAN, JAMES F.

AUTHORS: NADLER, LEE M.
TITLE: B7, A New Member Of The Ig Superfamily With
Unique Expression On Activated And Neoplastic B Cells
JOURNAL: The Journal of Immunology
VOLUME: 143
ISSUE: 8
PAGES: 2714-2722
DATE: 15-OCT-1989
RELEVANT RESIDUES IN SEQ ID NO: 2: From -26 to 262
US-08-147-772-2

Query Match 100.0%; Score 1149; DB 2; Length 288;
Best Local Similarity 100.0%; Pred. No. 7e-113;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 27 GLSHFCSGVIHVTKEVATLSGCHNVSVLELAQTRIVYQKEKKVLTMSGDMNIWPE 86
QY 61 YKQRTIFDITNNLSIVILALRPSDEGTVECVLVKYEKDAFKREHLAEVTLVKADFPPTS 120
DB 87 YKQRTIFDITNNLSIVILALRPSDEGTVECVLVKYEKDAFKREHLAEVTLVKADFPPTS 146
QY 121 ISDFRIPTSNIRRIICSTSGGPPPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLPF 180
DB 147 ISDFRIPTSNIRRIICSTSGGPPPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLPF 206
QY 181 NMTTNSFMCLIKYGHRLVNOTFNNTTKQEHFPDN 216
DB 207 NMTTNSFMCLIKYGHRLVNOTFNNTTKQEHFPDN 242

RESULT 2

US-08-456-104-6
Sequence 6, Application US/08456104
Patent No. 5861310
GENERAL INFORMATION:
APPLICANT: Freeman, Gordon J.
APPLICANT: Nadler, Lee M.
APPLICANT: Gray, Gary S.
TITLE OF INVENTION: TUMOR CELLS MODIFIED TO EXPRESS B7-2 AND B7-3 WITH INCREASED
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,104
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/101,624;
FILING DATE: 26-JUL-1993;
APPLICATION NUMBER: 08/109,393;
APPLICATION NUMBER: 19-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Mandragoras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: RPI-008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 288 amino acids